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<170> PatentIn version 3.1

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Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu

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Leu	Pro	Asp	Leu	Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr	
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Pro	Ile	Tyr	Tyr	Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	
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Phe	Ala	Ser	Tyr	Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val	Ala	Ala	
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Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465      470      475      480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt      1488
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<210> 11
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 <212> PRT
 <213> *Aspergillus niger*

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Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
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Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
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Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
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Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
165      170      175
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
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Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
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Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
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Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
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 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
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 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
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<211> 3697

<212> DNA

<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
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Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser			
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Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
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Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
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Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
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Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
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Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
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Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
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Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
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Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
      305      310      315      320
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
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Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
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Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
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Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
      370      375      380
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
      385      390      395      400
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
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Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
      420      425      430
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
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Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
      450      455      460
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
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<211> 3570
 <212> DNA
 <213> *Aspergillus niger*

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<210> 16
 <211> 1518
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 <213> *Aspergillus niger*

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 <221> CDS
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Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
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tac ttc cta ttg acg gat cgg ttc ggt agg acg gac aat tcg acg aca 144
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
35 40 45
gct aca tgc gat acg ggt gac caa atc tat tgt ggt ggc agt tgg caa 192
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
50 55 60
gga atc atc aac cat ctg gat tat atc cag ggc atg gga ttc acg gcc 240
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65 70 75 80
atc tgg atc tcg oct atc act gaa cag ctg ccc cag gat act gct gat 288
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
85 90 95
ggg gaa gct tac cat gga tat tgg cag cag aag ata tac gac gtg aac 336
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
100 105 110
tcc aac ttc ggc act gca gat gac ctc aag tcc ctc tca gat gcg ctt 384
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
115 120 125
cat gcc cgc gga atg tac ctc atg gtg gac gtc gtc cct aac cac atg 432
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
130 135 140
ggc tac gcc gcc aac ggc aac gat gta gac tac agc gtc ttc gac ccc 480
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
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ttc gat tcc tcc tcc tac ttc cac cca tac tgc ctg atc aca gat tgg 528
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
165 170 175
gac aac ttg acc atg gtc caa gat tgt tgg gag ggt gac acc atc gta 576
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
180 185 190
tct ctg cca gac cta aac acc acc gaa act gcc gtg aga aca atc tgg 624

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Tyr	Asp	Trp	Val	Ala	Asp	Leu	Val	Ser	Asn	Tyr	Ser	Val	Asp	Gly	Leu	
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Gln	Glu	Ala	Ala	Gly	Val	Tyr	Cys	Val	Gly	Glu	Val	Asp	Asn	Gly	Asn	
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cct	gcc	ctc	gac	tgc	cca	tac	cag	aag	gtc	ctg	gac	ggc	gtc	ctc	aac	816
Pro	Ala	Leu	Asp	Cys	Pro	Tyr	Gln	Lys	Val	Leu	Asp	Gly	Val	Leu	Asn	
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Tyr	Pro	Ile	Tyr	Trp	Gln	Leu	Leu	Tyr	Ala	Phe	Glu	Ser	Ser	Ser	Gly	
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Ser	Ile	Ser	Asn	Leu	Tyr	Asn	Met	Ile	Lys	Ser	Val	Ala	Ser	Asp	Cys	
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Arg	Phe	Ala	Ser	Tyr	Thr	Ser	Asp	Tyr	Ser	Gln	Ala	Lys	Asn	Val	Leu	
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agc	tac	atc	ttc	ctc	tcc	gac	ggc	atc	ccc	atc	gtc	tac	gcc	ggc	gaa	1056
Ser	Tyr	Ile	Phe	Leu	Ser	Asp	Gly	Ile	Pro	Ile	Val	Tyr	Ala	Gly	Glu	
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gaa	cag	cac	tac	tcc	ggc	ggc	aag	gtg	ccc	tac	aac	cgc	gaa	gcg	acc	1104
Glu	Gln	His	Tyr	Ser	Gly	Gly	Lys	Val	Pro	Tyr	Asn	Arg	Glu	Ala	Thr	
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Trp	Leu	Ser	Gly	Tyr	Asp	Thr	Ser	Ala	Glu	Leu	Tyr	Thr	Trp	Ile	Ala	
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Thr	Thr	Asn	Ala	Ile	Arg	Lys	Leu	Ala	Ile	Ser	Ala	Asp	Ser	Ala	Tyr	
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atg	cgc	aaa	ggc	acc	tca	ggg	agc	caa	gtc	atc	acc	gtc	ctc	tcc	aac	1296
Met	Arg	Lys	Gly	Thr	Ser	Gly	Ser	Gln	Val	Ile	Thr	Val	Leu	Ser	Asn	
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Lys	Gly	Ser	Ser	Gly	Ser	Ser	Tyr	Thr	Leu	Thr	Leu	Ser	Gly	Ser	Gly	
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Tyr	Thr	Ser	Gly	Thr	Lys	Leu	Ile	Glu	Ala	Tyr	Thr	Cys	Thr	Ser	Val	
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acc	gtg	gac	tcg	agc	ggc	gat	att	ccc	gtg	ccg	atg	gcg	tcg	gga	tta	1440
Thr	Val	Asp	Ser	Ser	Gly	Asp	Ile	Pro	Val	Pro	Met	Ala	Ser	Gly	Leu	
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Pro	Arg	Val	Leu	Leu	Pro	Ala	Ser	Val	Val	Asp	Ser	Ser	Ser	Leu	Cys	
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<211> 505

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<213> *Aspergillus niger*

<400> 17

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Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
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65      70      75      80
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
85      90      95
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
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Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
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His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
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180     185     190
Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
195     200     205
Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
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Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
245     250     255
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290     295     300
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355     360     365
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<213> *Penicillium chrysogenum*

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Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp	
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Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys	
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gca tac cat ctg atg caa caa cgc atc atc tcc aac cct cat gac atg	240
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met	
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Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu	
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Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr	
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acg gat ctt gat gtt cca tca gcc cag gaa gtc aag caa ctg egg tcc	384
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser	
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Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe	
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Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg	
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Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly	
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Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Leu Lys Lys Gln	
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Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu	
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Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala	
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Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu	
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Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro	
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Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala	
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Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln	
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Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu	
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Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe	
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Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His	
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Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu	
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Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu	
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His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu	
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Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr	
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<212> PRT

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 85 90 95
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 225 230 235 240
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 260 265 270
 Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly
 275 280 285
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 385 390 395 400
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 420 425 430
 Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu
 435 440 445
 Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro
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Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg
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85	Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln				
90	gtc ctc atg cct gat atc cgg aaa ctg cga gaa acg atc aag ccc agc	336			
100	Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser				
105	aac act aac aga ggc gat gcc atc tct tct att gtc att gcc atg cag	384			
110	Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln				
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180	Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu				
185	190	act ttt ctc cga agc ctg gct gag gac tgc gaa ggt gct tat gga acg	624		
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260	Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly				
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305	Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys				
310	315	320	ggg tac gag tac gga cgt acc gcg gtt cct atc gag caa acc gat gag	1008	
325	Gly Tyr Glu Tyr Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu				
330	335	aat gtt gca aat cta caa aca ttt gct ggt atg ggg ctg atc ggg ttc	1056		
340	Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe				
345	350	gtt cag aag gat cag tat gac cgg tac atg cat atg tca aac acg aat	1104		
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435	440	445	1392
act gtc tct ggc aag gtg gtg act gaa cat cga aac ctc cca agc gtg			
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val			
450	455	460	1440
gcg ttg aaa gat gcg atg agt aac tac gtg gac agc atg gat ttt gtc			
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val			
465	470	475	1488
acc aca aac gac gaa ggg caa gcc act gac gat ctc cca atc gac gag			
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu			
485	490	495	1536
tca ttc tca ccg tta ttg cac cgc atc gaa tca gca gtt cga tat cgt			
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg			
500	505	510	1584
gct gtg cat ccc aat gac cct gtc ctc gac ccc tca gag cgg ctc act			
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr			
515	520	525	1632
gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc cat			
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His			
530	535	540	1680
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag			
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys			
545	550	555	1728
aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca ggt			
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly			
565	570	575	1776
ttg gac gtg gac gcc ctg ctc agc ctc gaa ccc aag cga acg aag att			
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile			
580	585	590	1824
tcc acc gag aat gca atc cca gag ttc aag caa aca ctt tcc cgc gcg			
Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala			
595	600	605	1872
gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc			
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile			
610	615	620	1920
atc gag agc cag atc aca cac agc ctc ggt cat tca aat tac gac cgt			
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg			
625	630	635	1968
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag			
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu			
645	650	655	2016
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg			
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met			

660	665	670	
tgt cgg gag gag ctg ggt ggg gat cgg agg gag ctg tgg tgg ttt gta			2064
Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val			
675	680	685	
agg aag gga aag ctt ggg ctc att ggc aag agt gag gtg gat agc tcg			2112
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser			
690	695	700	
gct gtt gag gag caa gag gct caa gag ttt ctg gct ccc aat tga			2157
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn			
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<210> 23

<211> 718

<212> PRT

<213> *Penicillium chrysogenum*

<400> 23

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20 25 30	
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg	
35 40 45	
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr	
50 55 60	
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu	
65 70 75 80	
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln	
85 90 95	
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser	
100 105 110	
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln	
115 120 125	
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile	
130 135 140	
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly	
145 150 155 160	
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr	
165 170 175	
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu	
180 185 190	
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr	
195 200 205	
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr	
210 215 220	
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu	
225 230 235 240	
Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr	
245 250 255	
Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly	
260 265 270	
Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp	
275 280 285	
Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu	
290 295 300	
Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys	

